Qualimap Analysis Results

BAM QC analysis
Generated by Qualimap v.2.2.2-dev
2024/10/10 04:22:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617505.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR617505 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617505_1.fastq.gz SRR617505_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 04:22:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617505.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,304,212 / 94.7%
Unmapped reads	1,695,788 / 5.3%
Mapped paired reads	30,304,212 / 94.7%
Mapped reads, first in pair	15,311,713 / 47.85%
Mapped reads, second in pair	14,992,499 / 46.85%
Mapped reads, both in pair	29,680,604 / 92.75%
Mapped reads, singletons	623,608 / 1.95%
Secondary alignments	0
Supplementary alignments	162,680 / 0.51%
Read min/max/mean length	30 / 100 / 100.2
Duplicated reads (estimated)	6,203,570 / 19.39%
Duplication rate	9.89%
Clipped reads	6,084,872 / 19.02%

2.2. ACGT Content

Number/percentage of A's	869,460,895 / 29.52%
Number/percentage of C's	594,396,886 / 20.18%
Number/percentage of T's	868,865,075 / 29.5%
Number/percentage of G's	609,663,398 / 20.7%
Number/percentage of N's	2,769,232 / 0.09%

GC Percentage	40.88%

2.3. Coverage

Mean	0.9519
Standard Deviation	9.5869

2.4. Mapping Quality

Mean Mapping Quality	52.68

2.5. Insert size

Mean	40,702.38
Standard Deviation	1,885,310.6
P25/Median/P75	173 / 218 / 288

2.6. Mismatches and indels

General error rate	1.25%
Mismatches	35,927,893
Insertions	439,246
Mapped reads with at least one insertion	1.42%
Deletions	1,021,786
Mapped reads with at least one deletion	3.3%
Homopolymer indels	47.38%

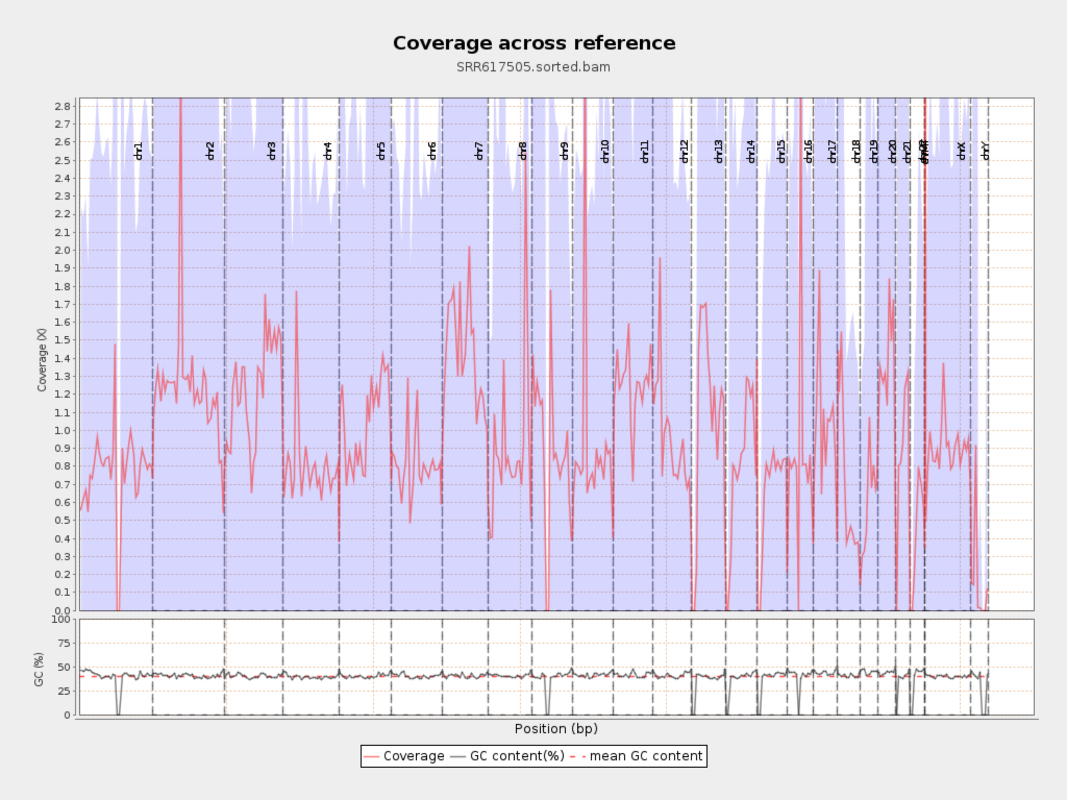
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

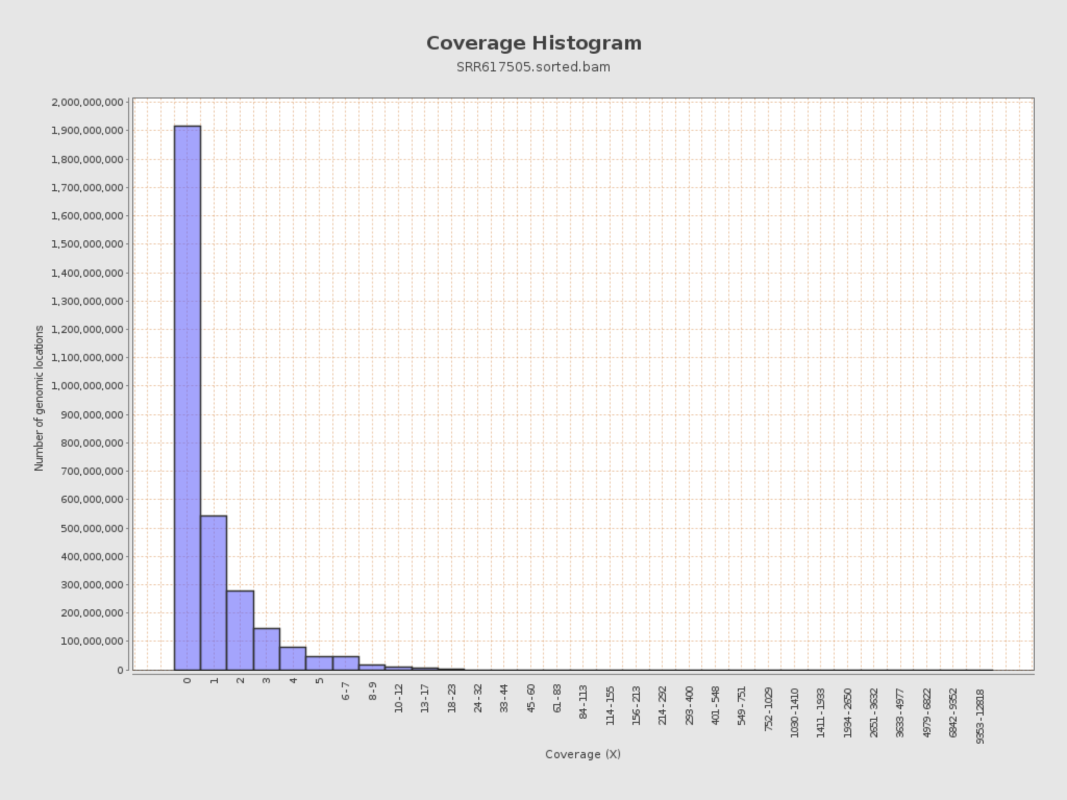
		bases	coverage	deviation
chr1	249250621	189768382	0.7614	9.3042
chr2	243199373	304559016	1.2523	11.2522
chr3	198022430	243553420	1.2299	2.2374
chr4	191154276	152434519	0.7974	6.0449
chr5	180915260	188929427	1.0443	2.0739
chr6	171115067	138979961	0.8122	5.3481
chr7	159138663	227021551	1.4266	13.0172
chr8	146364022	130950690	0.8947	3.834
chr9	141213431	121843702	0.8628	18.0705
chr10	135534747	124971943	0.9221	18.4871
chr11	135006516	166144702	1.2306	12.7355
chr12	133851895	128668172	0.9613	2.0208
chr13	115169878	124976628	1.0852	2.1278
chr14	107349540	85903424	0.8002	2.2066
chr15	102531392	66549277	0.6491	1.5429
chr16	90354753	79287971	0.8775	14.7079
chr17	81195210	82289248	1.0135	13.5382
chr18	78077248	52779911	0.676	16.7673
chr19	59128983	35184749	0.5951	5.756
chr20	63025520	86849862	1.378	2.7938
chr21	48129895	42475179	0.8825	3.7335
chr22	51304566	22038536	0.4296	1.2439
chrMT	16571	2070626	124.9548	88.5056
chrX	155270560	138489265	0.8919	4.0965

chrY	59373566	10174129	0.1714	13.2698

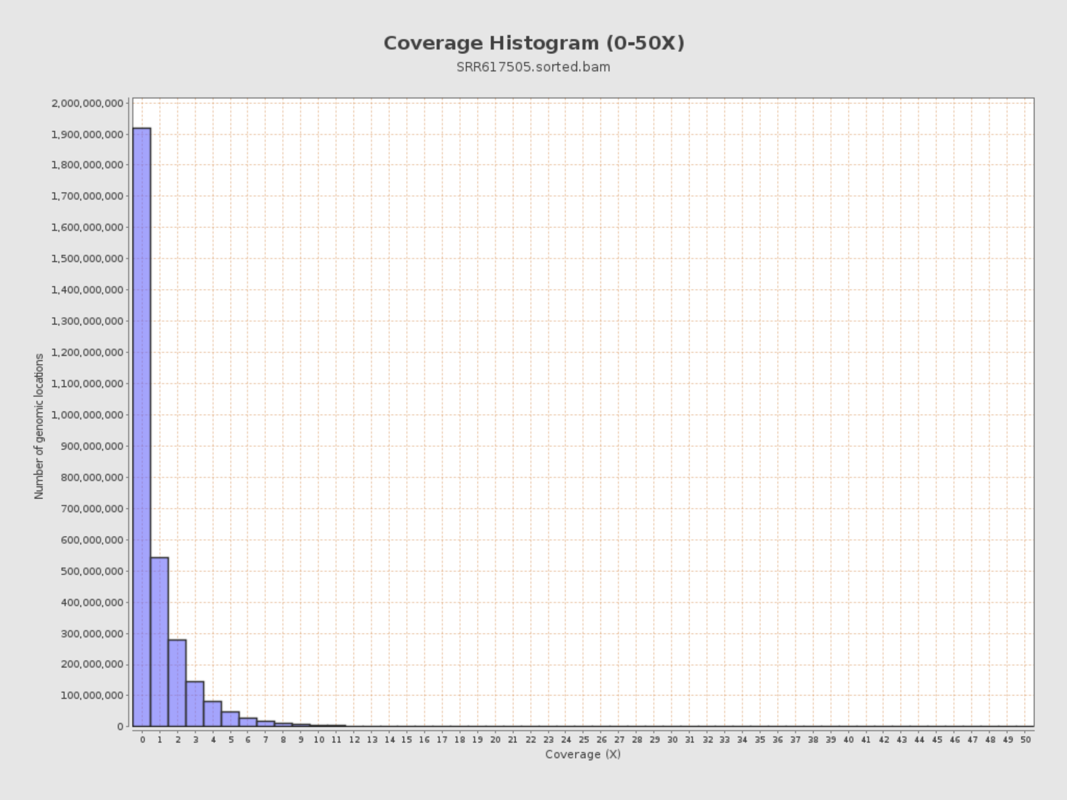
3. Results : Coverage across reference



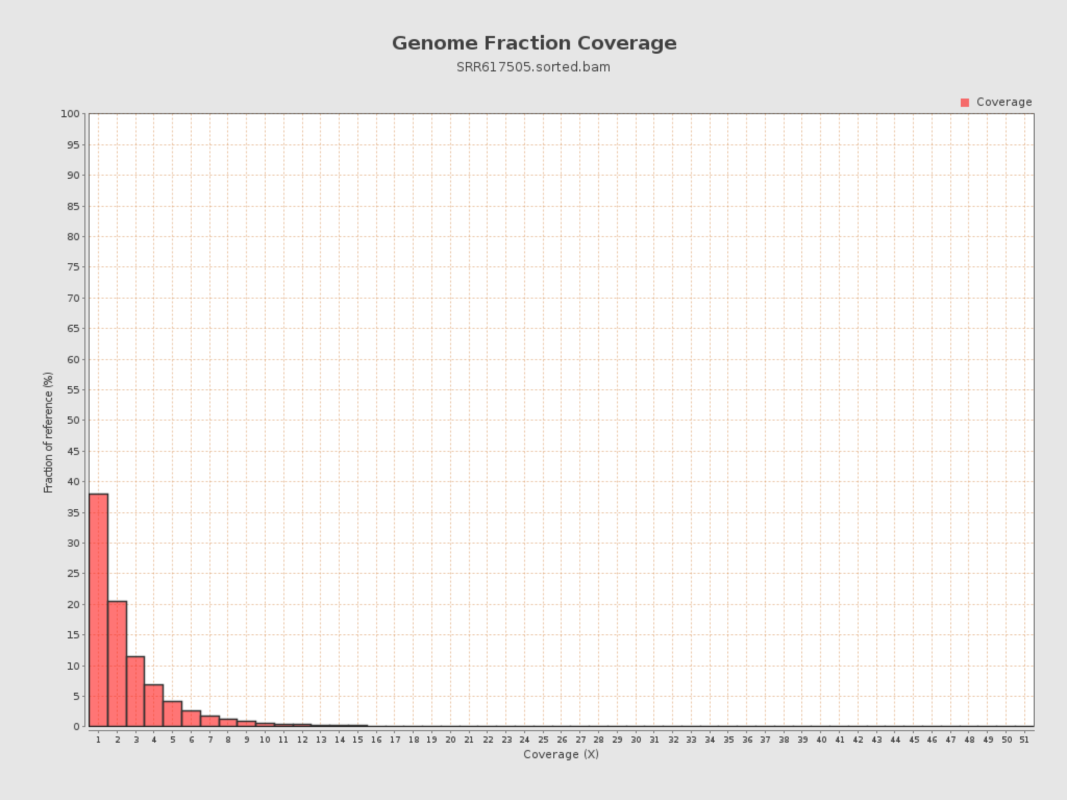
4. Results : Coverage Histogram



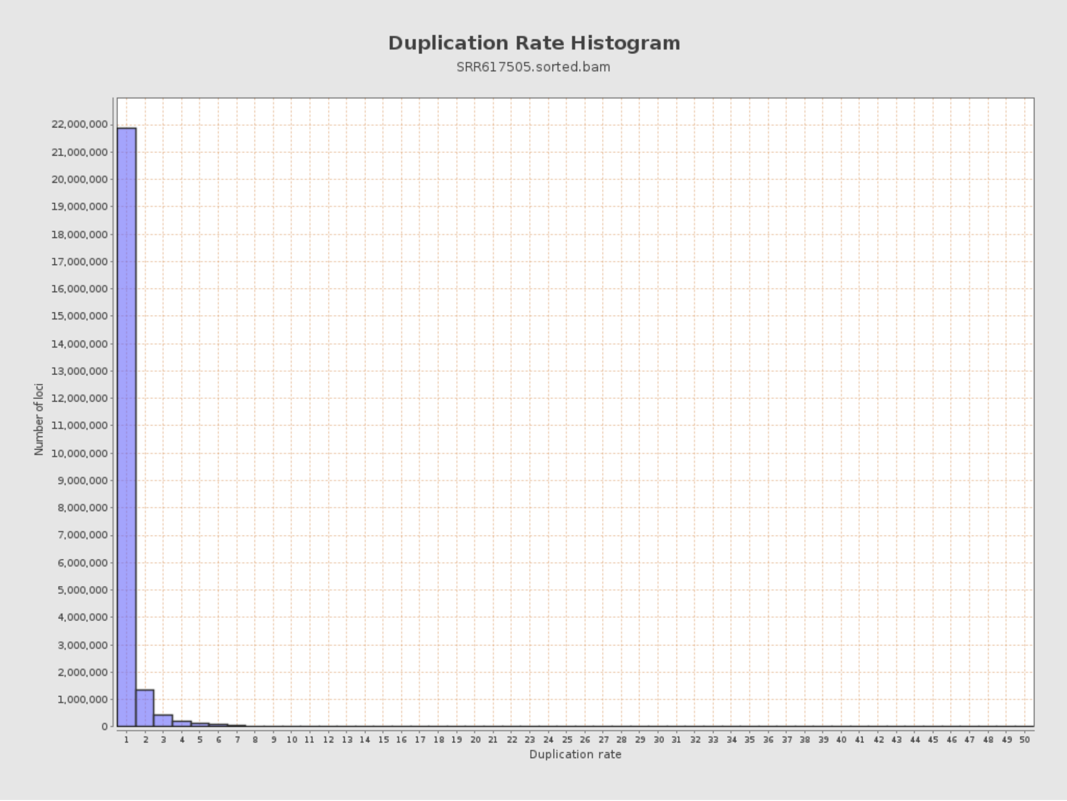
5. Results : Coverage Histogram (0-50X)



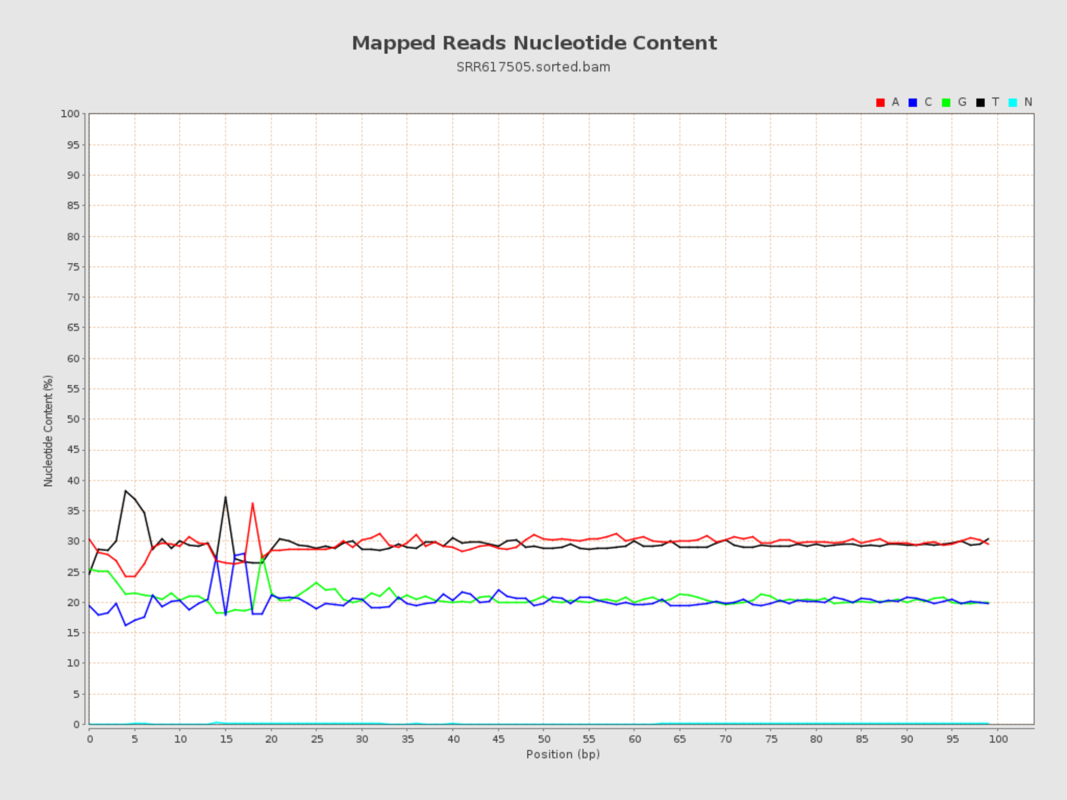
6. Results : Genome Fraction Coverage



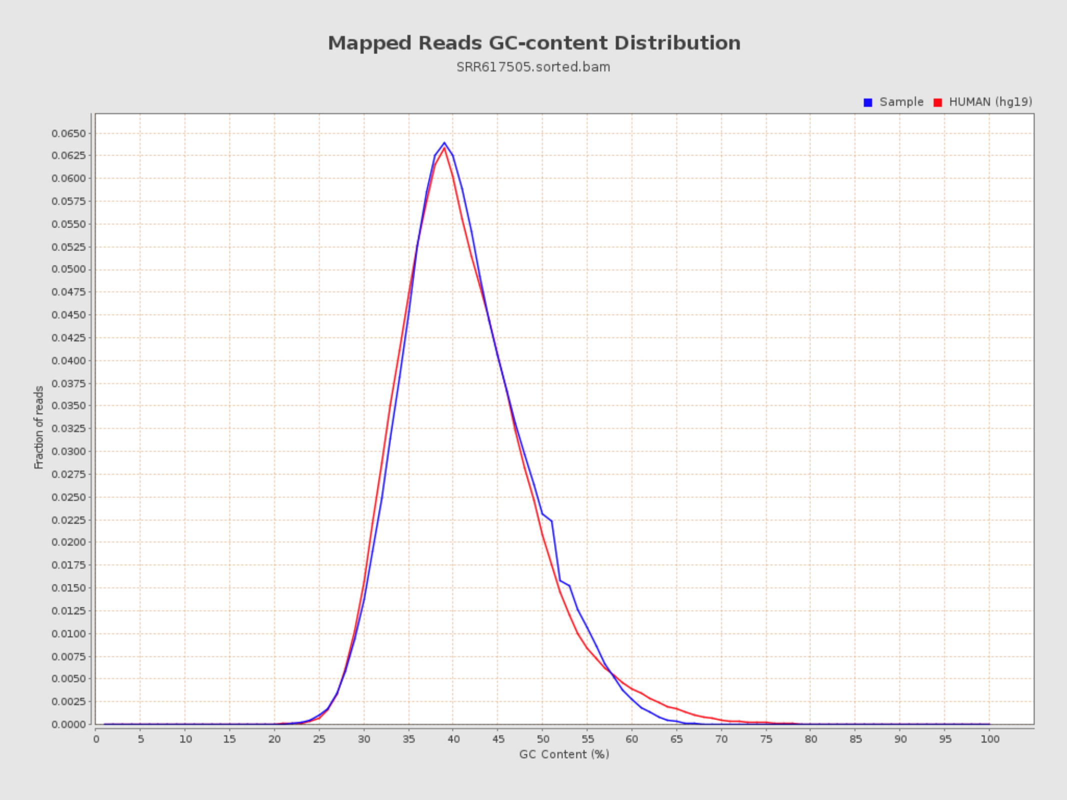
7. Results : Duplication Rate Histogram



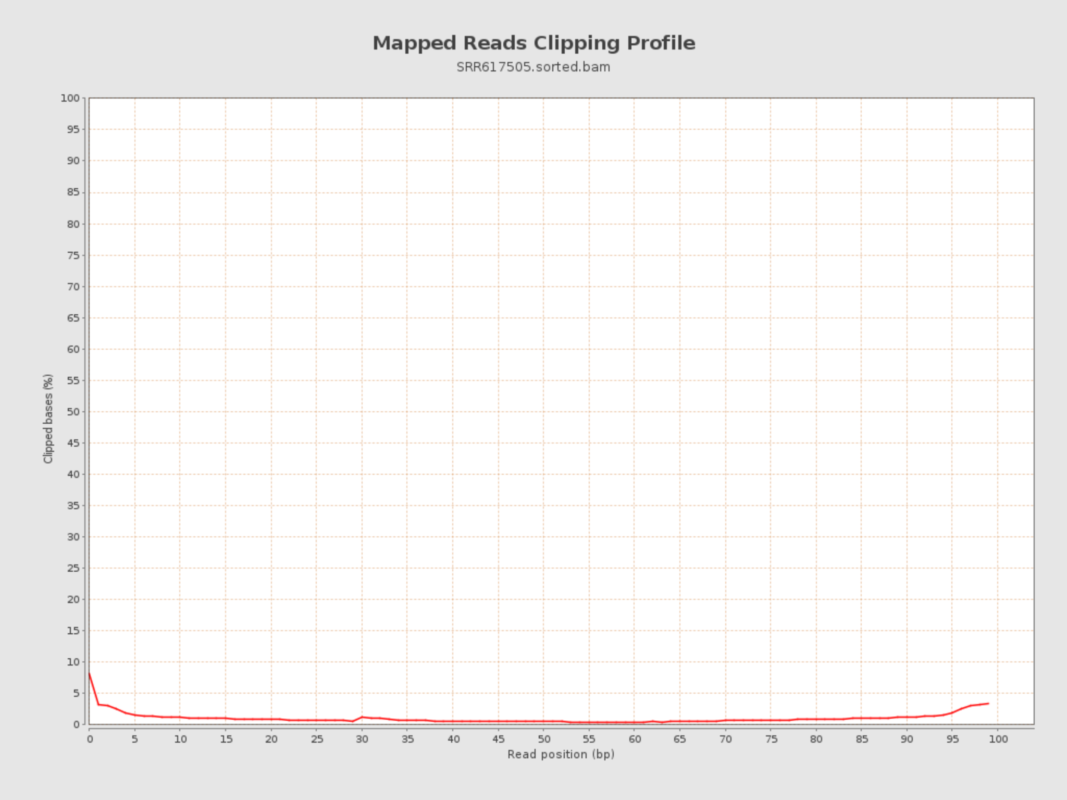
8. Results : Mapped Reads Nucleotide Content



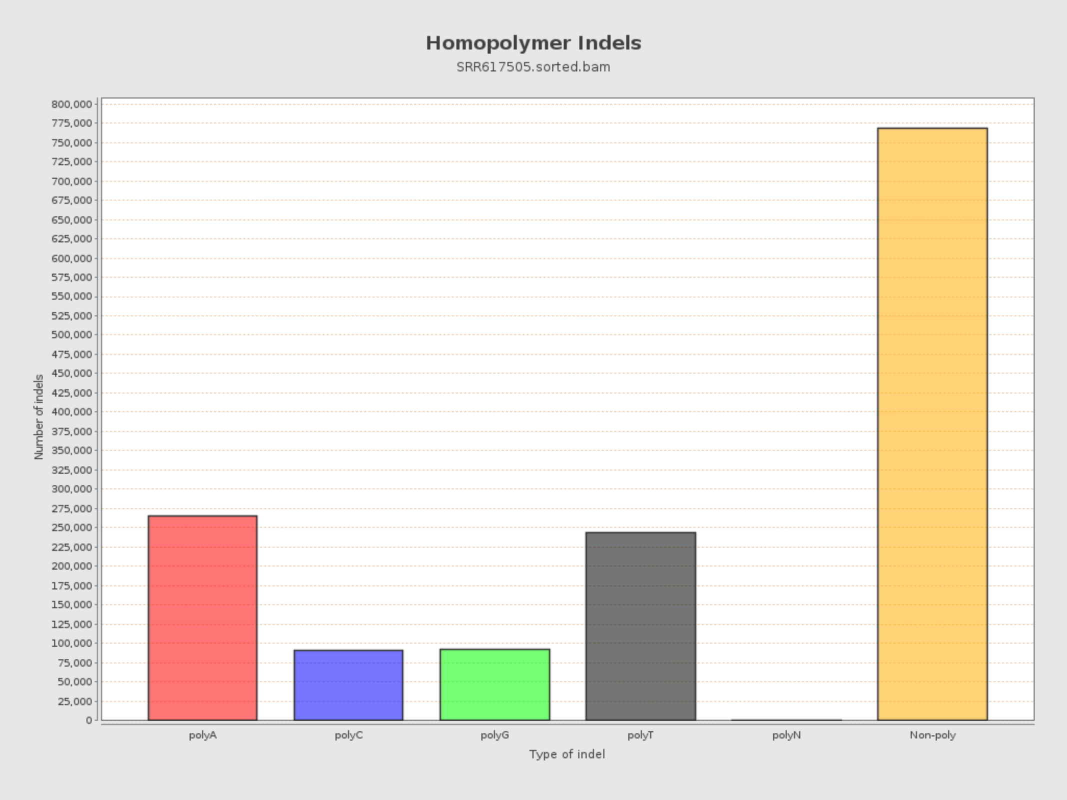
9. Results : Mapped Reads GC-content Distribution



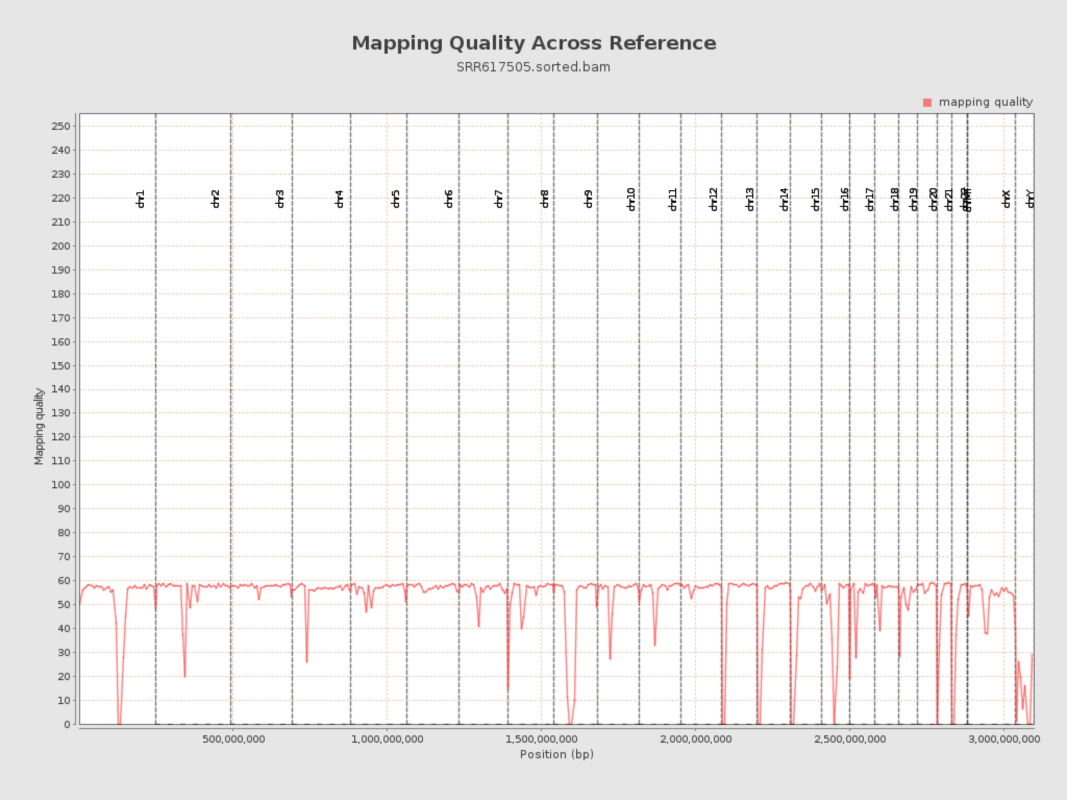
10. Results : Mapped Reads Clipping Profile



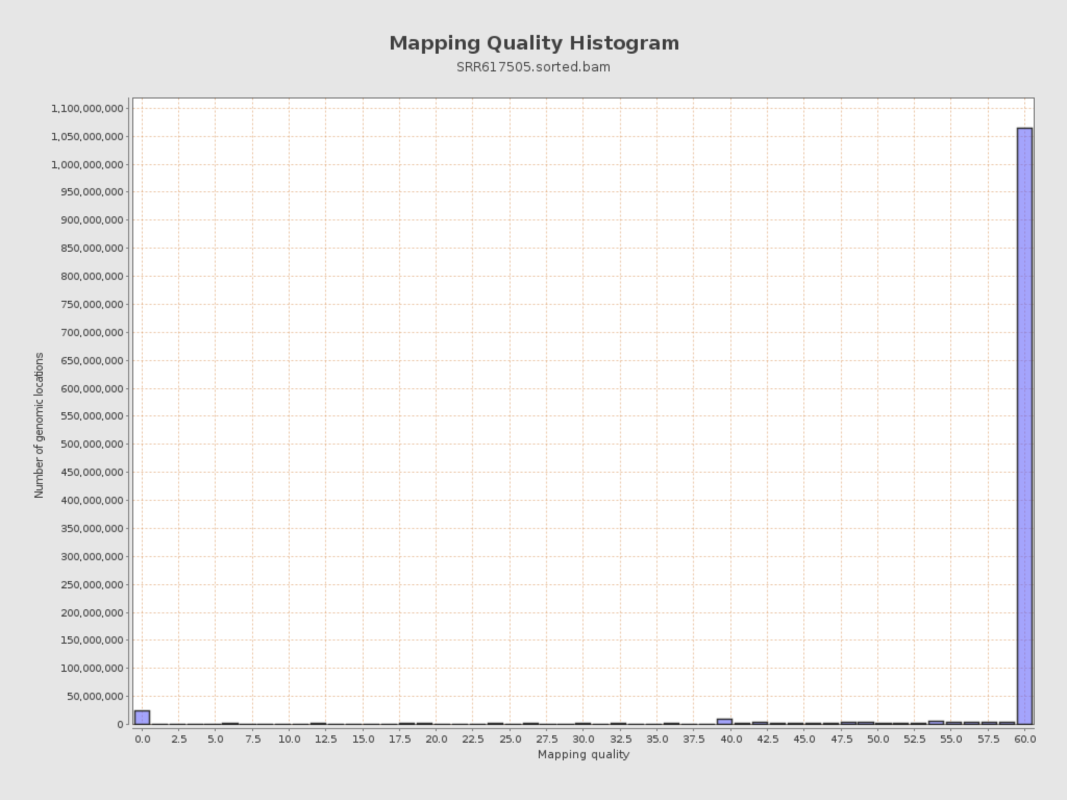
11. Results : Homopolymer Indels



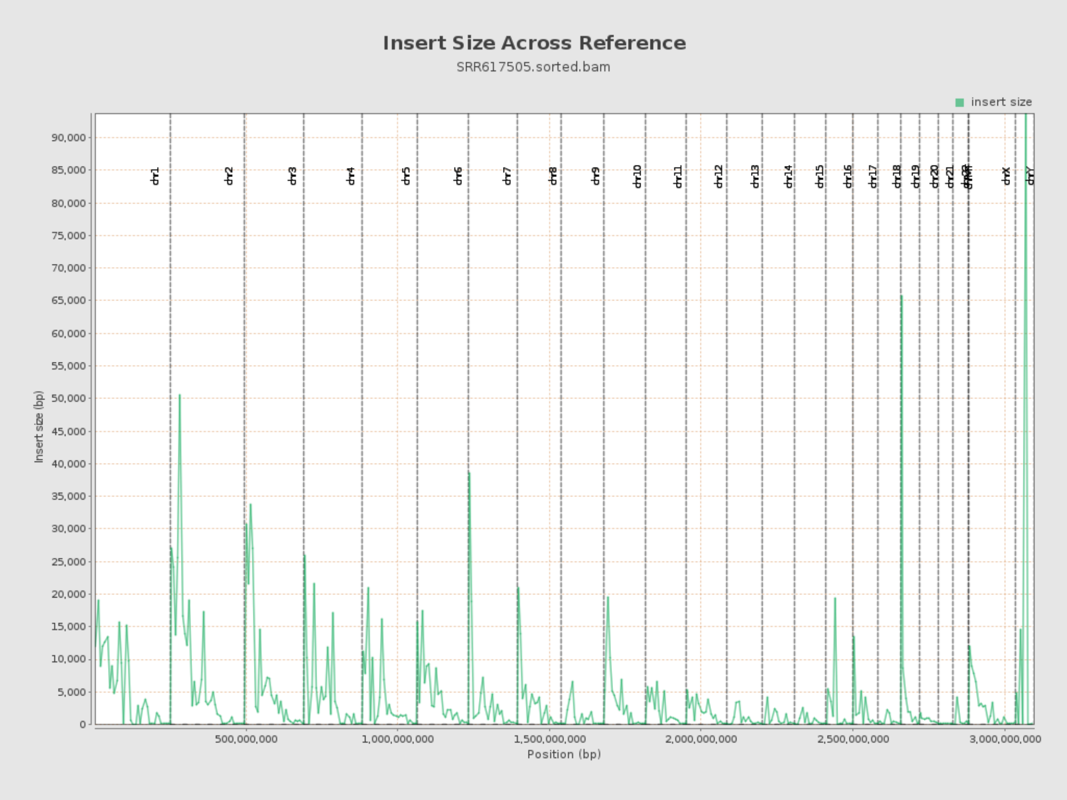
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram